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1

Lb 652 EGILLGDAVGKNEVLVVSALT 676

RESULT 14

amidase - Methanobacterium thermoautotrophium (strain Delta H)
C1Species: *Methanobacterium thermoautotrophium*
C1Strain: DSM 9746
C1Accession: D59066
R.Smith, D.R.Doreville, Stamm, L.A., DeLonghery, C.J., Lee, H., Dubois, J., Aldredge, T., Olin, E., Spallholz, P., Viscusi, G., Ward, F., Melnikow, J., Alston, P., Jensen, N.
Biol. Microbiol. 1987; 37(1):1-15.
J. Bacteriol. 179, 7185-7185, 1997
A1Title: Complete genome sequence of *Methanobacterium thermoautotrophium* delta H; functional
A1Reference number: A650003 | MIMD|98037514
A1Accession: D59066
A1Status: preliminary nucleic acid sequence not shown; translation not shown
A1Molecule type: DNA
A1Residues: 1-454 <MT>
A1Cross-references: strA; covin; strA; fcr0666; nitroreductase; hsdR; Aae571.1; fhs3; fhs4
A1Experimental source: strain Delta H
C1Genetics:
A1Gene: MTH496
A1Start codon: GTG
C1Superfamily: Indoleacetamide hydrolase

Query Match

```

Query Match      32.08,  Score 43.51,  DB 2,  Length 454;
Res+ Local Similarity 32.28;  Prod No. 32;
Matches 7,  Conservations 12,  Mismatches 6,  Index's 5,  Caps 1;

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2 DSCLELONMIST - FRILVOTLUSLS 20

DB 284 EGAIVELDFGYIDLCLPTYYLINVEFES 313

RESULT 19

cleavage and hydrolyzation specificity factor 100k chain - bovine
N.Material name(s): CFEF 100k chain
C.Species: Bos primigenius taurus (cattle)
Cloned sequence accession number: AF069718.1; EMBL:AF069718.1; F069718.1; GenBank:U05419.7
Accession: A56351
Benny, A.; Haari, H.P.; Keller, W.
Mol. Cell. Biol. 14: 8193-8197, 1994
Affile characterization of cellular and post-translational specificity factor and cloning
A.Reference number: A56351, MIMD:95059047
Accession: A56351
A.Status: preliminary, nucleic acid sequence not shown
A.Molecule type: mRNA
A.Pos:pos: 1..782 <END>
Access.references: JBX:K75931; NID:q959037; PID:q959683
A.Note: Parts of this sequence were confirmed by peptide sequencing

Query: Match

Query Match:	32.00	Score 43.5	28 2	Length 793
Best Local Similarity	34.58	Pred. No. 58		
Matches 10; Conservative	5	Mismatches 7	Indels 7	Gaps 1

4 CILLQ-----MDFGFQKHLVDFLOSL 255

Db 20 CYLQVDEHRELLQCGWDEHFSM.IIDSL 48

